

B

CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA 120

(8EQ ID No: 37)

Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro  
10 15 20

Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala

Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu

Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr  
55 60 65 70

Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His

Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp  
90 95 100

Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met  
105 110 115

Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val  
120 125 130

Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp  
135 140 145 150

Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His  
155 160 165

Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr  
170 175 180

FIGURE 1 (Con't)

CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG	751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser <u>Asn</u> Met	
185 190 195	
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC	799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr	
200 205 210	
CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA	847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val	
215 220 225 230	
CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC	895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile	
235 240 245	
AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC	943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys <u>Asn</u>	
250 255 260	
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA	991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
265 270 275	
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC	1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u>	
280 285 290	
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC	1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
295 300 305 310	
AAA GTT CAG GAC ATA GAC T GAGACTCAT TCGTGGAACA TTAGCATGGA	1136
Lys Val Gln Asp Ile Asp	
315	
TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA	1196
CTAAGAGACA TGGCCACCGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG	1256
TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTTCATG GTGATTACAC AACGGTTTTA	1316
CAATTTTGTA ATGATTTCCCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG	1376
AAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT	1436
GTGCCACTGA GAACCTTGAA ATTAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT	1496
GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCCTGGGA CCTGCAAATA AGTTCTTTTT	1556

FIGURE 1 (Con't)

TTCTAATGAG	GAGAGAAAAA	TATATGTATT	TTTATATAAT	GTCTAAAGTT	ATATTTTCAGG	1616
TGTAATGTTT	TCTGTGCAAA	GTTTTGTAAA	TTATATTTGT	GCTATAGTAT	TTGATTCAAA	1676
ATATTTAAAA	ATGTCTCACT	GTTGACATAT	TTAATGTTTT	AAATGTACAG	ATGTATTTAA	1736
CTGGTGCACT	TTGTAATTCC	CCTGAAGGTA	CTCGTAGCTA	AGGGGGCAGA	ATACTGTTTC	1796
TGGTGACCAC	ATGTAGTTTA	TTTCTTTATT	CTTTTAACT	TAATAGAGTC	TTCAGACTTG	1856
TCAAACTAT	GCAAGCAAAA	TAAATAAATA	AAAATAAAAT	GAATACCTTG	AATAATAAGT	1916
AGGATGTTGG	TCACCAGGTG	CCTTTCAAAT	TTAGAAGCTA	ATTGACTTTA	GGAGCTGACA	1976
TAGCCAAAAA	GGATACATAA	TAGGCTACTG	AAATCTGTCA	GGAGTATTTA	TGCAATTATT	2036
GAACAGGTGT	CTTTTTTTAC	AAGAGCTACA	AATTGTAAAT	TTTGTTTCTT	TTTTTTCCCA	2096
TAGAAAATGT	ACTATAGTTT	ATCAGCCAAA	AAACAATCCA	CTTTTAAATT	TAGTGAAAGT	2156
TATTTTATTA	TACTGTACAA	TAAAAGCATT	GTCTCTGAAT	GTTAATTTTT	TGGTACAAAA	2216
AATAAATTTG	TACGAAAACC	TGAAAAAAA	AAAAA	AAAAAAGGG	CGGCCGCTCT	2276
AGAGGGCCCT	ATTCTATAG					2295

## Expression of 32D-F3 in COS-7 Cells

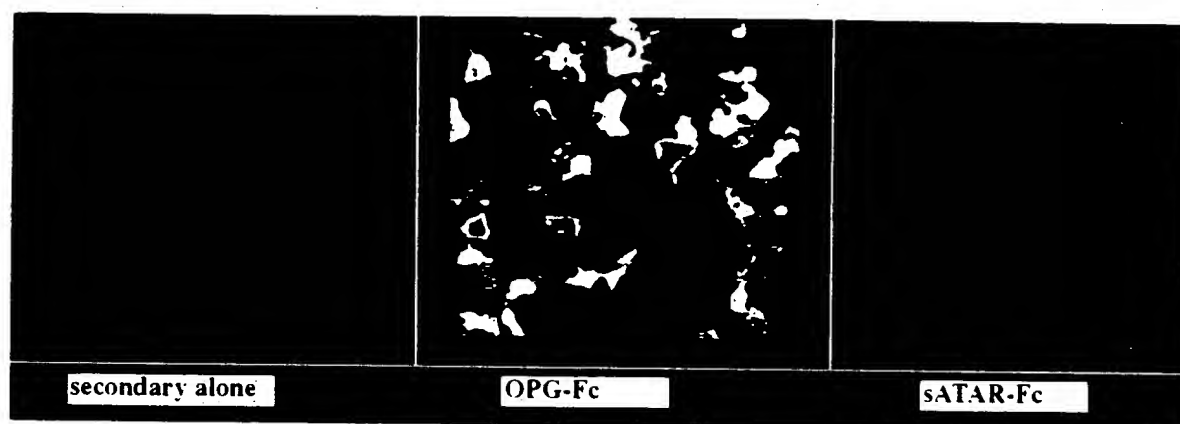


FIGURE 2

# OPG Binding Protein Expression in Human Tissues

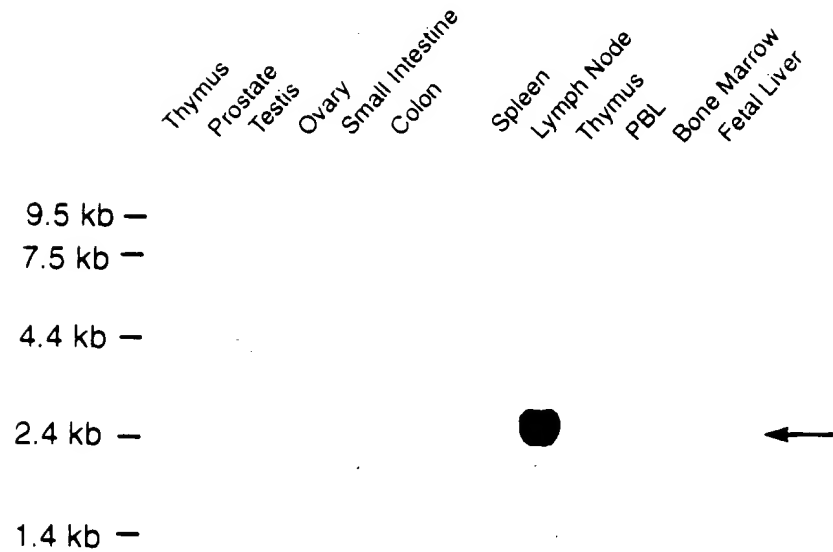


FIGURE 3

FIGURE 4

B (Seq ID No: 38)

10 30 50  
AAGCTTGGTACCGAGCTCGGATCCACTACTCGACCCACGCGTCCGCGCGCCCCAGGAGCC

70 90 110  
AAAGCCGGGCTCCAAGTCGGCGCCCCACGTCGAGGCTCCGCCGCAGCCTCCGGAGTTGGC

130 150 170  
CGCAGACAAGAAGGGGAGGGAGCGGGAGAGGGAGGAGAGCTCCGAAGCGAGAGGGCCGAG

190 210 230  
CGCCATGCGCCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGG

B (Seq ID No: 39) M R R A S R D Y T K Y L R G S E E M G

250 270 290  
CGGCGGCCCCGGAGCCCCGCACGAGGGCCCCCTGCACGCCCCGCCGCCCTGCGCCGCA  
G G P G A P H E G P L H A P P P P A P H

310 330 350  
CCAGCCCCCGCCGCCCTCCCGCTCCATGTTCTGTTGGCCCTCCTGGGGCTGGGGCTGGGCCA  
Q P P A A S R S M F V A L L G L G L G Q

370 390 410  
GGTTGTCTGCAGCGTCGCCCTGTTCTTCTATTTTCAGAGCGCAGATGGATCCTAATAGAAT  
V V C S V A L F F Y F R A Q M D P N R I

430 450 470  
ATCAGAAGATGGCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTT  
S E D G T H C I Y R I L R L H E N A D F

490 510 530  
TCAAGACACAACCTCTGGAGAGTCAAGATACAAAATTAATACCTGATTTCATGTAGGAGAAT  
Q D T T L E S Q D T K L I P D S C R R I

550 570 590  
TAAACAGGCCTTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA  
K Q A F Q G A V Q K E L Q H I V G S Q H

610 630 650  
CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCAAGAGGAGCAA  
I R A E K A M V D G S W L D L A K R S K

670 690 710  
GCTTGAAGCTCAGCCTTTTGTCTCATCTCACTATTAATGCCACCGACATCCCATCTGGTTC  
L E A Q P F A H L T I N A T D I P S G S

730 750 770  
CCATAAAGTGAGTCTGTCTCTTGGTACCATGATCGGGGTTGGGCCAAGATCTCCAACAT  
H K V S L S S W Y H D R G W A K I S N M

790 810 830  
GACTTTTAGCAATGGAAAACCTAATAGTTAATCAGGATGGCTTTTATTACCTGTATGCCAA  
T F S N G K L I V N Q D G F Y Y L Y A N

850 870 890  
CATTTGCTTTTCGACATCATGAAACTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAAT  
I C F R H H E T S G D L A T E Y L Q L M

910 930 950  
GGTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCGTGATGAAAGGAGG  
V Y V T K T S I K I P S S H T L M K G G

970 990 1010

GenBank

FIGURE 4

AAGCACCAAGTATTGGTCAGGGAATTCTGAATTCATTTTATTCCATAAACGTTGGTGG  
 S T K Y W S G N S E F H F Y S I N V G G  
  
 1030 1050 1070  
 ATTTTAAAGTTACGGTCTGGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACT  
 F F K L R S G E E I S I E V S N P S L L  
  
 1090 1110 1130  
 GGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTTCGAGATATAGATTGAGC  
 D P D Q D A T Y F G A F K V R D I D  
  
 1150 1170 1190  
 CCCAGTTTTTGGAGTGTATGTATTTCCCTGGATGTTTGAAACATTTTTTAAACAAGCC  
  
 1210 1230 1250  
 AAGAAAGATGTATATAGGTGTGTGAGACTACTAAGAGGCATGGCCCCAACGGTACACGAC  
  
 1270 1290 1310  
 TCAGTATCCATGCTCTTGACCTTGTAGAGAACACGCGTATTTACAGCCAGTGGGAGATGT  
  
 1330 1350 1370  
 TAGACTCATGGTGTGTTACACAATGGTTTTTAAATTTTGTAAATGAATTCCTAGAAATTA  
  
 1390 1410 1430  
 CCAGATTGGAGCAATTACGGGTGACCTTATGAGAACTGCATGTGGGCTATGGGAGGGG  
  
 1450 1470 1490  
 TTGGTCCCCTGGTCATGTGCCCCCTTCGCAGCTGAAGTGGAGAGGGTGTCTATCTAGCGCAAT  
  
 1510 1530 1550  
 TGAAGGATCATCTGAAGGGGCAAATTCCTTTTGAATTGTTACATCATGCTGGAACCTGCAA  
  
 1570 1590 1610  
 AAAAATACTTTTCTAATGAGGAGAGAGAAAATATATGTATTTTATATAATATCTAAAGTTA  
  
 1630 1650 1670  
 TATTTTCAGATGTAATGTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT  
  
 1690 1710 1730  
 TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTAAATGTACAGA  
  
 1750 1770 1790  
 CATATTTAACTGGTGCACTTTGTAAATTCCTGGGGAAAACTTGCAGCTAAGGAGGGGAA

GenBank: E07676

**FIGURE 4**

1810 1830 1850  
AAAAATGTTGTTTCCTAATATCAAATGCAGTATATTCTTCGTTCTTTTAAAGTTAATAG

1870 1890 1910  
ATTTTTTTCAGACTTGTCAAGCCGTGTGCAAAAAAATTAAAAATGGATGCCTTGAATAATAAG

1930 1950 1970  
CAGGATGTTGGCCACCAGGTGCCTTTCAAATTTAGAAACTAATTGACTTTTAGAAAGCTGA

1990 2010 2030  
CATTGCCAAAAAGGATACATAATGGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG

2050 2070 2090  
TTGAACAGGTGTTTTTCCACAAGTGCCGCAAATGTACCTTTTTTTTTTTTTTCAAAATAG

2110 2130 2150  
AAAAGTTATTAGTGGTTTATCAGCAAAAAAGTCCAATTTTAATTTAGTAAATGTTATCTT

2170 2190 2210  
ATACTGTACAATAAAAAACATTGCCTTTGAATGTTAATTTTTTGGTACAAAAATAAATTTA

2230 2250 2270  
TATGAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGGCCCTATTCTATAG

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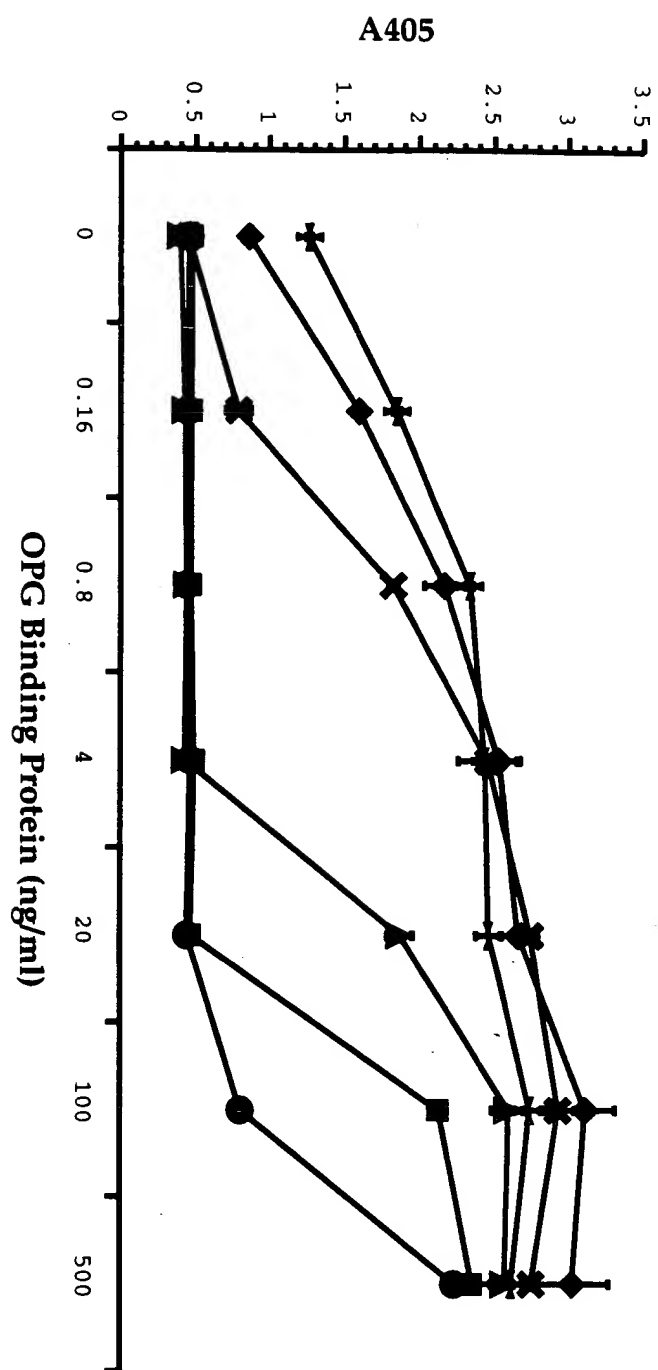


FIGURE 8

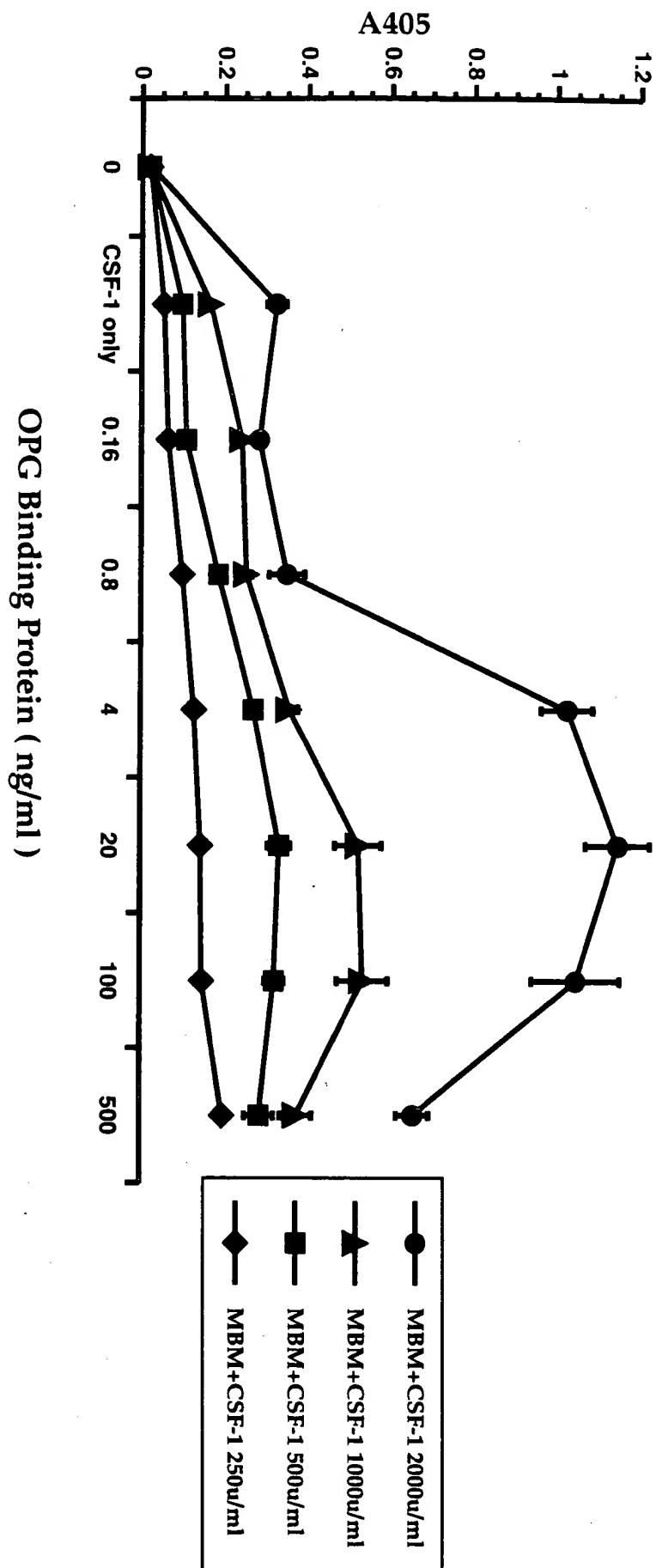
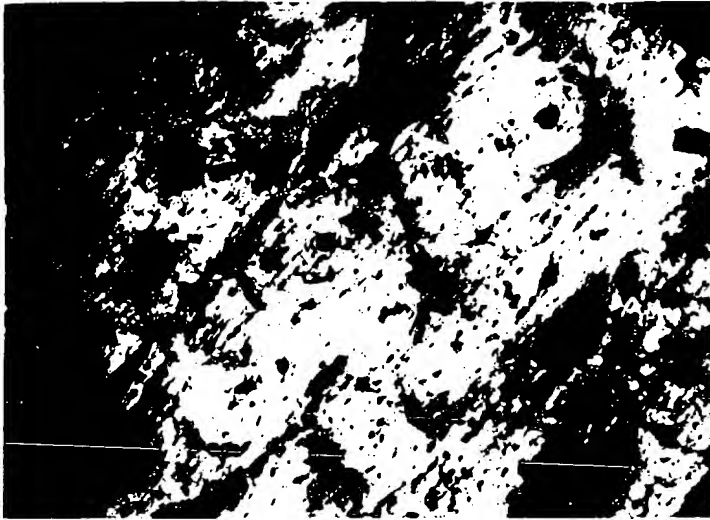
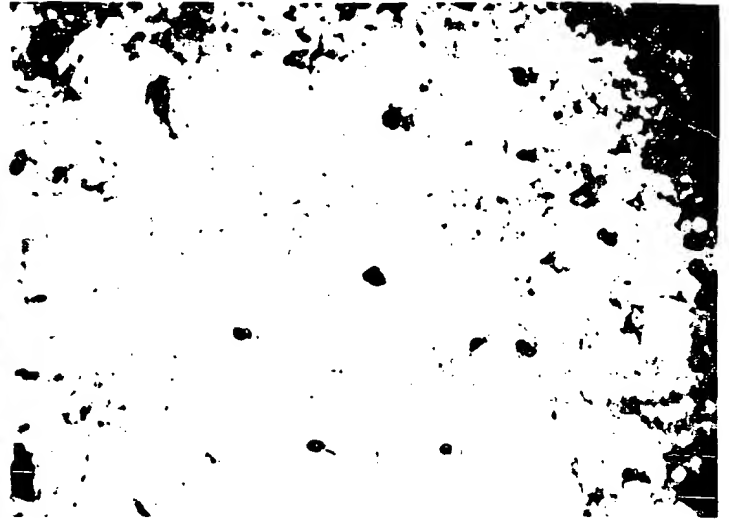


FIGURE 6

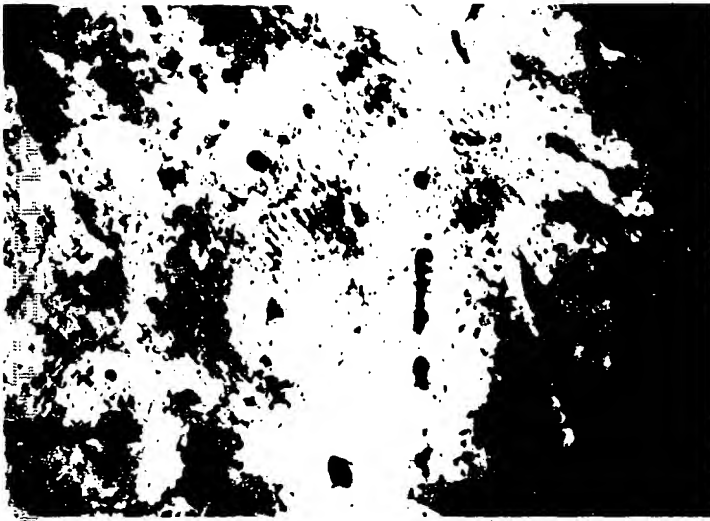
**Toluidine Blue Staining**



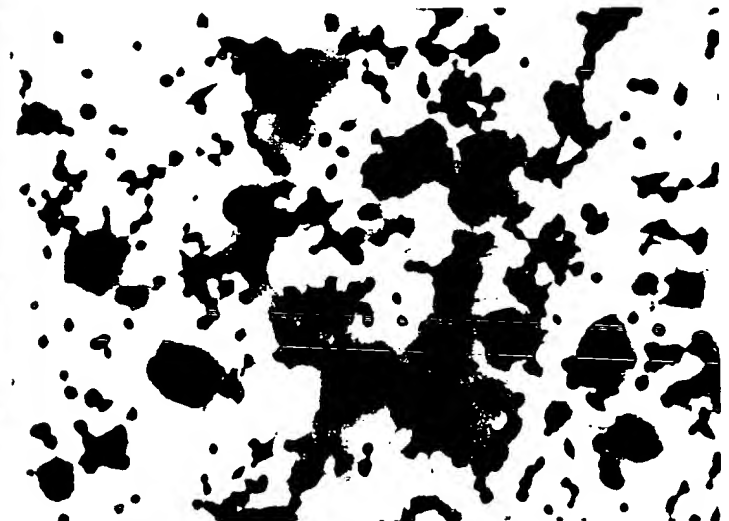
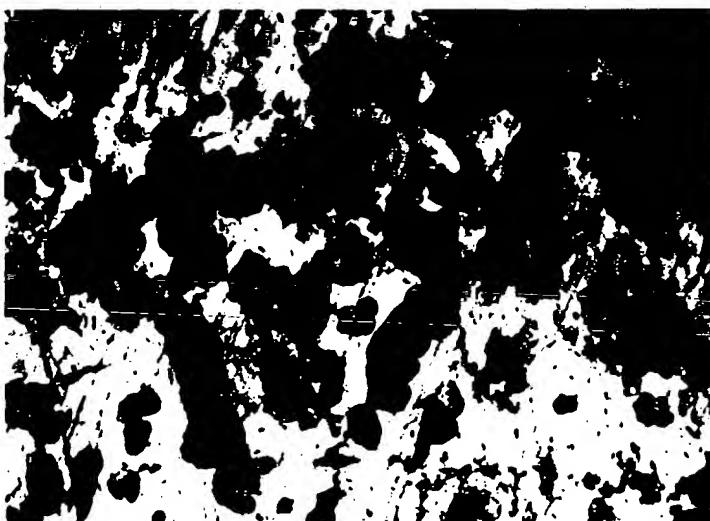
**TRAP staining**



**Bone Marrow Cells + M-CSF-1**



**Bone Marrow Cells + OPG Binding Protein**



**Bone Marrow Cells + M-CSF-1 + OPG Binding Protein**

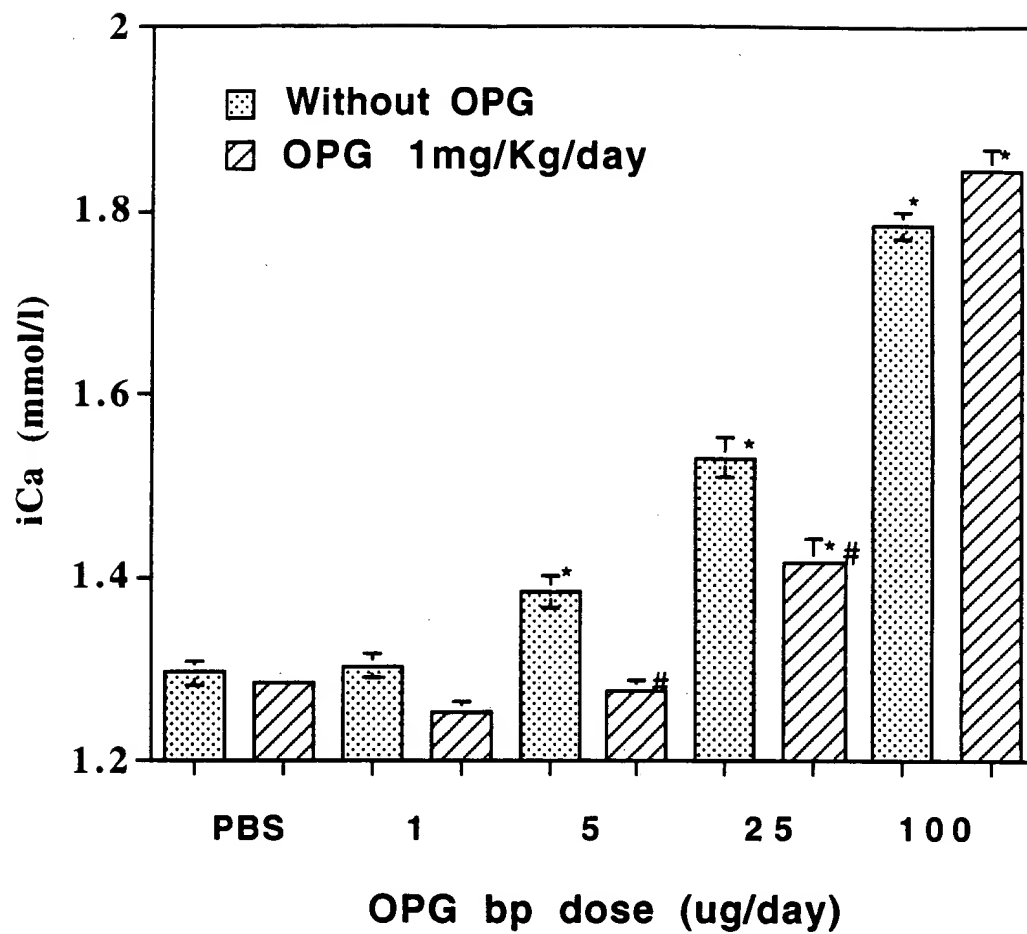


FIGURE 8

**PBS**



**OPGbp 5ug/d**



**OPGbp 25ug/d**



**OPGbp100ug/d**



FIGURE 9